

K. Haude

PAGE: 1

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/206,132

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DATE: 10/23/2000  
TIME: 23:00:55

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OCT 30 2000

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

TECH CENTER 1600/2800

#11

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P.2.

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT: Freeman, Gordon J.  
Nadler, Lee M.  
Gray, Gary S.

(ii) TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3  
WITH INCREASED IMMUNOGENICITY AND USES THEREFOR

(iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: LAHIVE & COCKFIELD  
(B) STREET: 60 State Street, Suite 510  
(C) CITY: Boston  
(D) STATE: Massachusetts  
(E) COUNTRY: USA  
(F) ZIP: 02109

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/206,132  
(B) FILING DATE:  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/456,104  
(B) FILING DATE:  
(A) APPLICATION NUMBER: 08/101,624  
(B) FILING DATE: 26-JUL-1993  
(A) APPLICATION NUMBER: 08/109,393  
(b) FILING DATE: 19-AUG-1993

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Mandragouras, Amy E.  
(B) REGISTRATION NUMBER: 36,207  
(C) REFERENCE/DOCKET NUMBER: RPI-008

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/206,132DATE: 10/23/2000  
TIME: 23:00:56

INPUT SET: S36032.raw

47 (ix) TELECOMMUNICATION INFORMATION:  
48 (A) TELEPHONE: (617) 227-7400  
49 (B) TELEFAX: (617) 227-5941  
50  
51  
52

53 (2) INFORMATION FOR SEQ ID NO:1:  
54

55 (i) SEQUENCE CHARACTERISTICS:  
56 (A) LENGTH: 1120 base pairs  
57 (B) TYPE: nucleic acid  
58 (C) STRANDEDNESS: single  
59 (D) TOPOLOGY: linear  
60

61 (ii) MOLECULE TYPE: cDNA  
62  
63

64 (ix) FEATURE:  
65 (A) NAME/KEY: CDS  
66 (B) LOCATION: 107..1093  
67  
68

69 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
70

71	CACAGGGTGA AAGCTTTGCT TCTCTGCTGC TGTAACAGGG ACTAGCACAG ACACACGGAT	60
72		
73	GAGTGGGGTC ATTTCCAGAT ATTAGGTCAC AGCAGAAGCA GCCAAA ATG GAT CCC	115
74		Met Asp Pro
75		1
76		
77	CAG TGC ACT ATG GGA CTG AGT AAC ATT CTC TTT GTG ATG GCC TTC CTG	163
78	Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu	
79	5 10 15	
80		
81	CTC TCT GGT GCT GCT CCT CTG AAG ATT CAA GCT TAT TTC AAT GAG ACT	211
82	Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr	
83	20 25 30 35	
84		
85	GCA GAC CTG CCA TGC CAA TTT GCA AAC TCT CAA AAC CAA AGC CTG AGT	259
86	Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser	
87	40 45 50	
88		
89	GAG CTA GTA GTA TTT TGG CAG GAC CAG GAA AAC TTG GTT CTG AAT GAG	307
90	Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu	
91	55 60 65	
92		
93	GTA TAC TTA GGC AAA GAG AAA TTT GAC AGT GTT CAT TCC AAG TAT ATG	355
94	Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met	
95	70 75 80	
96		
97	GGC CGC ACA AGT TTT GAT TCG GAC AGT TGG ACC CTG AGA CTT CAC AAT	403
98	Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn	
99	85 90 95	

100																	
101	CTT	CAG	ATC	AAG	GAC	AAG	GGC	TTG	TAT	CAA	TGT	ATC	ATC	CAT	CAC	AAA	451
102	Leu	Gln	Ile	Lys	Asp	Lys	Gly	Leu	Tyr	Gln	Cys	Ile	Ile	His	His	Lys	
103	100					105					110					115	
104																	
105	AAG	CCC	ACA	GGA	ATG	ATT	CGC	ATC	CAC	CAG	ATG	AAT	TCT	GAA	CTG	TCA	499
106	Lys	Pro	Thr	Gly	Met	Ile	Arg	Ile	His	Gln	Met	Asn	Ser	Glu	Leu	Ser	
107					120					125					130		
108																	
109	GTG	CTT	GCT	AAC	TTC	AGT	CAA	CCT	GAA	ATA	GTA	CCA	ATT	TCT	AAT	ATA	547
110	Val	Leu	Ala	Asn	Phe	Ser	Gln	Pro	Glu	Ile	Val	Pro	Ile	Ser	Asn	Ile	
111				135				140						145			
112																	
113	ACA	GAA	AAT	GTG	TAC	ATA	AAT	TTG	ACC	TGC	TCA	TCT	ATA	CAC	GGT	TAC	595
114	Thr	Glu	Asn	Val	Tyr	Ile	Asn	Leu	Thr	Cys	Ser	Ser	Ile	His	Gly	Tyr	
115			150					155					160				
116																	
117	CCA	GAA	CCT	AAG	AAG	ATG	AGT	GTT	TTG	CTA	AGA	ACC	AAG	AAT	TCA	ACT	643
118	Pro	Glu	Pro	Lys	Lys	Met	Ser	Val	Leu	Leu	Arg	Thr	Lys	Asn	Ser	Thr	
119		165				170						175					
120																	
121	ATC	GAG	TAT	GAT	GGT	ATT	ATG	CAG	AAA	TCT	CAA	GAT	AAT	GTC	ACA	GAA	691
122	Ile	Glu	Tyr	Asp	Gly	Ile	Met	Gln	Lys	Ser	Gln	Asp	Asn	Val	Thr	Glu	
123	180				185						190					195	
124																	
125	CTG	TAC	GAC	GTT	TCC	ATC	AGC	TTG	TCT	GTT	TCA	TTC	CCT	GAT	GTT	ACG	739
126	Leu	Tyr	Asp	Val	Ser	Ile	Ser	Leu	Ser	Val	Ser	Phe	Pro	Asp	Val	Thr	
127					200					205					210		
128																	
129	AGC	AAT	ATG	ACC	ATC	TTC	TGT	ATT	CTG	GAA	ACT	GAC	AAG	ACG	CGG	CTT	787
130	Ser	Asn	Met	Thr	Ile	Phe	Cys	Ile	Leu	Glu	Thr	Asp	Lys	Thr	Arg	Leu	
131				215					220				225				
132																	
133	TTA	TCT	TCA	CCT	TTC	TCT	ATA	GAG	CTT	GAG	GAC	CCT	CAG	CCT	CCC	CCA	835
134	Leu	Ser	Ser	Pro	Phe	Ser	Ile	Glu	Leu	Glu	Asp	Pro	Gln	Pro	Pro	Pro	
135			230					235					240				
136																	
137	GAC	CAC	ATT	CCT	TGG	ATT	ACA	GCT	GTA	CTT	CCA	ACA	GTT	ATT	ATA	TGT	883
138	Asp	His	Ile	Pro	Trp	Ile	Thr	Ala	Val	Leu	Pro	Thr	Val	Ile	Ile	Cys	
139		245				250					</						

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/206,132DATE: 10/23/2000  
TIME: 23:00:57

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153 GAT GAA GCC CAG CGT GTT TTT AAA AGT TCG AAG ACA TCT TCA TGC GAC 1075  
154 Asp Glu Ala Gln Arg Val Phe Lys Ser Ser Lys Thr Ser Ser Cys Asp  
155 310 315 320  
156

157 AAA AGT GAT ACA TGT TTT TAATTAAAGA GTAAAGCCCA AAAAAAA 1120  
158 Lys Ser Asp Thr Cys Phe  
159 325  
160  
161

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

165 (A) LENGTH: 329 amino acids  
166 (B) TYPE: amino acid  
167 (D) TOPOLOGY: linear  
168

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

172  
173 Met Asp Pro Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met  
174 1 5 10 15  
175  
176 Ala Phe Leu Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe  
177 20 25 30  
178  
179 Asn Glu Thr Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln  
180 35 40 45  
181  
182 Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val  
183 50 55 60  
184  
185 Leu Asn Glu Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser  
186 65 70 75 80  
187  
188 Lys Tyr Met Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg  
189 85 90 95  
190  
191 Leu His Asn Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile  
192 100 105 110  
193  
194 His His Lys Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser  
195 115 120 125  
196  
197 Glu Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile  
198 130 135 140  
199  
200 Ser Asn Ile Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile  
201 145 150 155 160  
202  
203 His Gly Tyr Pro Glu Pro Lys Lys Met Ser Val Leu Leu Arg Thr Lys  
204 165 170 175  
205

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/206,132DATE: 10/23/2000  
TIME: 23:00:57

INPUT SET: S36032.raw

206 Asn Ser Thr Ile Glu Tyr Asp Gly Ile Met Gln Lys Ser Gln Asp Asn  
207 180 185 190  
208  
209 Val Thr Glu Leu Tyr Asp Val Ser Ile Ser Leu Ser Val Ser Phe Pro  
210 195 200 205  
211  
212 Asp Val Thr Ser Asn Met Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys  
213 210 215 220  
214  
215 Thr Arg Leu Leu Ser Ser Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln  
216 225 230 235 240  
217  
218 Pro Pro Pro Asp His Ile Pro Trp Ile Thr Ala Val Leu Pro Thr Val  
219 245 250 255  
220  
221 Ile Ile Cys Val Met Val Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys  
222 260 265 270  
223  
224 Lys Lys Arg Pro Arg Asn Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu  
225 275 280 285  
226  
227 Arg Glu Glu Ser Glu Gln Thr Lys Lys Arg Glu Lys Ile His Ile Pro  
228 290 295 300  
229  
230 Glu Arg Ser Asp Glu Ala Gln Arg Val Phe Lys Ser Ser Lys Thr Ser  
231 305 310 315 320  
232  
233 Ser Cys Asp Lys Ser Asp Thr Cys Phe  
234 325  
235

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1151 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 99..1028

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

252  
253  
254 GGAGCAAGCA GACGCGTAAG ACTGGCTCCT GTAGGCAGCA CGGACTTGAA CAACCAGACT 60  
255  
256 CCTGTAGACG TGTTCCAGAA CTTACGGAAG CACCCACG ATG GAC 104  
257 Met Asp  
258 1

PAGE: 1

**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/09/206,132**

DATE: 10/23/2000  
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**INPUT SET: S36032.raw**

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